

34. (Reiterated) The method of Claim 32, wherein the protein crystal belongs to the space group P4<sub>2</sub>1<sub>2</sub> with unit cell dimensions of a equals about 105 Å, b equals about 105 Å and c equals about 47 Å.

35. (Reiterated) The method of Claim 30, wherein said three-dimensional model is displayed as a set of atomic coordinates, a physical three-dimensional model, an image on a computer screen, a picture of said model or a set of coordinates derived from a picture of said model.

#### REMARKS

The Office communication states the Preliminary Amendment filed on September 10, 2002, is non-responsive because original Claims 1-3, drawn to the elected invention (three-dimensional models of a human IgE Fc region and methods of making such models), were canceled and new claims (21-39) were submitted that the Examiner believes are drawn to a non-elected invention. In particular, the Examiner states new claims 21-27 are drawn to a crystallographic data processing system, new claims 28 and 29 are drawn to a method of using such a system, new claims 30-35 are drawn to a method of displaying crystallographic data, and new claims 36-39 are drawn to methods of using crystallographic data to identify inhibitory compounds.

Applicants have canceled claims 36-39, drawn to methods of using crystallographic data to identify inhibitory compounds.

With regard to claims 21-35, Applicants respectfully disagree that these claims are directed to a non-elected invention; however, Applicants have amended these claims in an effort to remove any confusion as to the invention being claimed. Specifically, claim 21 has been amended to more clearly state the intended use of the data processing system. Similarly, claim 30 has been amended to more clearly state what is being displayed, namely the three-dimensional model.

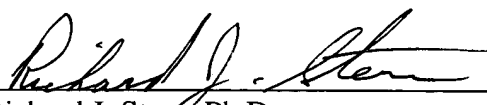
In the Restriction Requirement mailed July 18, 2002, the claims were divided into 10 restriction groups. Group I, containing claims 1-3, was directed to three-dimensional models of the Fc-region of human IgE protein and methods of producing such models as well as methods of producing three-dimensional models of the Fc-region from IgE proteins other than human proteins.

Applicants submit claims 21-35 are directed to the same subject matter as original claims 1-3 except that the new claims have been amended to include a recitation of the data structures encoded on a computer-readable medium allowing the functionality of the data structures to be realized. Additionally, the new claims recite a processing means further enhancing the functional interrelationship between the data structure and the other claimed aspects of the invention. While the language of the original and newly submitted claims differ, if one compares the individual steps of the model claims with the data processing claims, it can be seen the claims cover the same subject matter. In particular, claims 21-27 cover the subject matter of original claim 1, namely three-dimensional models of the Fc-region of IgE protein. New claims 28 and 29 cover the same subject matter as original claim 3, namely a method to produce a three-dimensional model of an Fc-region from an IgE protein other than a human IgE protein using the data processing system of claim 22. New claims 30-35 cover the same subject matter as original claim 2, namely a method to produce a three-dimensional model of the Fc-region of the human IgE protein. Applicants note the new claims and the amendments to them were drafted to comply with the Examination Guidelines for Computer-Related Inventions published by the patent office.

In summary, Applicants submit that the present claims are directed to elected Group I and request that the claims be examined. The Examiner is invited to contact the undersigned should any issues remain.

Respectfully submitted,

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VERSION WITH MARKINGS SHOWING CHANGES

Claims 36-39 have been canceled.

Claims 21- have been amended as follows:

21. (Once amended) A data processing system for producing a three-dimensional model of the Ce3 or Ce4 domain from an Fc-region of an IgE protein, said system comprising:

(a) a data storage medium encoding data representing atomic X-ray crystallographic coordinates, wherein said atomic coordinates define the relative position of amino acids from at least a portion of the Ce3 or Ce4 domain from the Fc-region of an IgE protein;

(b) a processing means, wherein said processing means transforms said data into a model representing at least a portion of the Ce3 or Ce4 domain from the Fc-region of an IgE protein.

22. (Reiterated) The data processing system of Claim 21, wherein said IgE protein is a human IgE protein.

23. (Reiterated) The data processing system of Claim 21, wherein said data represents the atomic coordinates of protein backbone atoms having a root mean square deviation less than 10 angstroms from the human IgE protein Ce3 or Ce4 domain backbone atoms defined by the atomic coordinates represented in Table 1, Table 2 or Table 3.

24. (Reiterated) The data processing system of Claim 21, wherein said data represents the atomic coordinates of backbone atoms from a protein having an amino acid sequence at least 80% homologous to the amino acid sequence of SEQ ID NO:2.

25. (Reiterated) The data processing system of Claim 21, wherein said data represents at least a portion of the atomic coordinates listed in Table 1, Table 2 or Table 3.

26. (Reiterated) The data processing system of Claim 21, wherein said data consists of the atomic coordinates listed in Table 1, Table 2 or Table 3.

27. (Reiterated) The data processing system of Claim 21 further comprising a display means for displaying said model.

28. (Reiterated) A method to produce a three-dimensional model of the Ce3 or Ce4 domain of the Fc-region of a non-human IgE protein, said method comprising:

- (a) obtaining a three-dimensional model of the Ce3 or Ce4 domain from the Fc-region of the human IgE protein using the data processing system of Claim 22;
- (b) obtaining the amino acid sequence of a non-human IgE protein;
- (c) comparing the Ce3 or Ce4 domain amino acid sequence from the non-human IgE protein with the Ce3 or Ce4 domain amino acid sequence from the human IgE protein;
- (d) at positions at which the two sequences differ, replacing the amino acids in the three-dimensional model of the human IgE with the amino acid from the corresponding position of the non-human IgE protein sequence to create a three-dimensional model of the non-human IgE protein; and
- (e) displaying said three-dimensional model of the non-human protein on a display means.

29. (Reiterated) The method of Claim 28, wherein said three-dimensional model of the human IgE protein is obtained using the atomic coordinates listed in Table 1, Table 2 or Table 3.

30. (Once amended) A method to produce a three-dimensional model of the Ce3 or the Ce4 domain of the Fc-region of the human IgE protein, said method comprising:

- (a) obtaining a first set of data representing the atomic x-ray crystallographic coordinates that define the relative position of amino acids from at least a portion of the Ce3 or Ce4 domain from the Fc-region of the human IgE protein;
- (b) transforming said first set of data into a second set of data representing a three-dimensional model; and
- (c) displaying said [data representing said] three-dimensional model represented by said second-set of data using a display means.

31. (Reiterated) The method of Claim 30, wherein the crystallographic coordinates of (a) are selected from Table 1, Table 2 or Table 3.

32. (Reiterated) The method of Claim 30, wherein said first set of data is obtained by the steps of:

- (i) obtaining a protein crystal comprising at least the Ce3 or at least the Ce4 domain from the Fc region of the human IgE protein;
- (ii) producing diffraction data from said protein crystal; and

(iii) transforming said diffraction data into data representing atomic coordinates of said protein comprising at least the Ce3 or at least the Ce4 domain from the Fc region of the human IgE protein.

33. (Reiterated) The method of Claim 32, wherein the protein crystal is produced using the hanging drop or the vapor diffusion method, wherein the protein comprising the Ce3 or Ce4 domain from the Fc-region of the human IgE protein is concentrated in a solution comprising about 10 mM Tris-(hydroxymethyl)aminomethane at about pH 8.0, and crystallization is performed using a precipitant composed of about 25 mM sodium acetate at a pH of about 4.6 and 33% polyethylene glycol 4000.

34. (Reiterated) The method of Claim 32, wherein the protein crystal belongs to the space group  $P4_212$  with unit cell dimensions of  $a$  equals about 105 Å,  $b$  equals about 105 Å and  $c$  equals about 47 Å.

35. (Reiterated) The method of Claim 30, wherein said three-dimensional model is displayed as a set of atomic coordinates, a physical three-dimensional model, an image on a computer screen, a picture of said model or a set of coordinates derived from a picture of said model.